UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE

INVITAE CORPORATION, *Plaintiff*, v. NATERA, INC., *Defendant*.	)	Case No. _____ **JURY TRIAL DEMANDED**

COMPLAINT FOR PATENT INFRINGEMENT

Plaintiff Invitae Corporation ("Invitae" or "Plaintiff") for its complaint against Defendant Natera, Inc. ("Natera" or "Defendant") alleges as follows:

NATURE OF THE ACTION

1. This action arises under 28 U.S.C. §§ 1331 and the United States Patent Act, 35. U.S.C. § 100 *et seq.*

2. Plaintiff brings this action to halt Natera's infringement of U.S. Patent Nos. 11,149,308 ("the '308 Patent") (attached hereto as Exhibit 1) and 11,155,863 ("the '863 Patent") (attached hereto as Exhibit 2) pursuant to its rights under the Patent Laws of the Unites States, 35 U.S.C. § 1, *et seq.*

THE PARTIES

3. Invitae is a corporation organized and existing under the laws of the State of Delaware, and is the owner of the '308 and '863 Patents pursuant to an assignment agreement recorded on August 31, 2021 and appearing at Reel/Frame Nos. 057344/0723 and 057343/0279, respectively, of the USPTO Patent Assignment Database.

4. Invitae is a leading medical genetics company whose mission is to bring comprehensive genetic information into mainstream medicine to improve healthcare for billions of people. Invitae's goal is to aggregate the world's genetic tests into a single service with higher quality, faster turnaround time, and lower prices.

5. On information and belief, Natera is a company organized and existing under the laws of Delaware, with its principal place of business at 201 Industrial Rd., San Carlos, California 94070. Natera provides a non-invasive test for minimal residual disease that it markets under the tradename "Signatera™." On information and belief, Natera performs the Signatera™ test at its facility in San Carlos, California.

JUSRISDICTION AND VENUE

6. This action arises under the Patent Laws of the United States of America, 35 U.S.C. § 1 *et seq.* This Court has federal question jurisdiction under 28 U.S.C. § 1331 and 28 U.S.C. § 1338(a) because this is a civil action arising under the Patent Act.

7. This Court has personal jurisdiction over Natera because Natera is incorporated in Delaware. Natera has purposefully availed itself of the benefits and protections of Delaware state law by incorporating under Delaware law.

8. This Court also has jurisdiction over Natera because Natera has availed itself of this forum, initiating civil actions in this jurisdiction, including *Natera, Inc. v. ArcherDX, Inc., et al.*, C.A. 20-125 LPS (D. Del. 2020).

9. Venue is proper in this District under 28 U.S.C. §§ 1391(b) and (c), and 1400(b) because Natera is a Delaware corporation, and Delaware is a convenient forum for resolution of the parties' disputes set forth herein.

BACKGROUND

10. Plaintiff repeats and re-alleges the foregoing paragraphs as if set forth specifically herein.

11. The '308 Patent is entitled "Sequence Assembly," and the claimed inventions were invented by Gregory Porreca and Caleb Kennedy, leading researchers in DNA sequencing technology and genomics. The '308 Patent claims and discloses novel techniques for improving the performance of DNA sequencing technology by allowing researchers to better extract the full scope of available information that results from modern DNA sequencing platforms so that mutations in an individual's DNA can be identified with enhanced specificity.

12. The '863 Patent is entitled "Sequence Assembly," and the claimed inventions were invented by Gregory Porreca and Caleb Kennedy, leading researchers in DNA sequencing technology and genomics. The '863 Patent claims and discloses novel techniques for improving the performance of DNA sequencing technology by allowing researchers to better extract the full scope of available information that results from modern DNA sequencing platforms so that mutations in an individual's DNA can be identified with enhanced specificity.

13. As the '308 and '863 Patents explain, "[n]ext-generation sequencing (NGS) technologies include instruments capable of sequencing more than 10^{14} kilobase-pair (kbp) of DNA per instrument run. Sequencing typically produces a large number of independent reads, each representing anywhere between 10 to 1000 bases of the nucleic acid." Ex. 1 at 1:31-36; Ex. 2 at 1:31-36. To determine whether the DNA carries a mutation, however, these "independent reads" must be reassembled into stretches of DNA sequence of sufficient length to reveal the presence of the mutation.

14. As the '308 and '863 Patents explain, prior art techniques for utilizing such DNA sequence information were "problematic," and suffered from accuracy problems such that it was impossible to detect certain kinds of key mutations using DNA sequencing technology:

> Another sequence assembly technique involves aligning each individual read to a reference. This assembly technique is problematic because very short reads (e.g., 50 bp or less) may align well in a number of places on a very long reference (e.g., 5 million bp). With a number of equally good positions to align to, aligning a read to a reference offers little positional accuracy. Also, particularly with very short reads, long indels can be difficult or impossible to detect.

Ex. 1 at 2:10-17; Ex. 2 at 2:10-17.

15. Likewise, the '308 and '863 Patents explain that existing techniques for reassembling the independent sequence reads did a "poor job" of interpreting certain kinds of mutations:

> Existing methods of read assembly do not offer the positional accuracy of a contig-based alignment while including detailed information from each read. Further, due to limitations in alignment algorithms, existing methods do a poor job of correctly interpreting certain mutations (e.g., indels near the ends of reads, substitutions near indels).

Ex. 1 at 2:24-29; Ex. 2 at 2:24-29. More specifically, the '308 and '863 Patents explain that existing techniques imposed an undesirable trade-off between detecting different kinds of mutations:

> Existing approaches to alignment involve algorithms with good mismatch sensitivity at the expense of indel sensitivity or good indel sensitivity at the expense of mismatch sensitivity. For example, if an alignment is to detect mismatches with sufficient fidelity, then it is likely that some indels will be missed.

Ex. 1 at 1:65-2:3; Ex. 2 at 1:65-2:3.

16. In view of these problems, the '308 Patent teaches and claims a new technique for improving DNA sequencing technology by enhancing sequence read assembly. Representative claim 1 of the '308 Patent is listed below:

> 1. A method for accurately identifying differences between a reference human

> genome and sequence reads obtained from a biological sample, the biological sample obtained from a human subject, the method comprising:
>
> > obtaining nucleic acid from the biological sample obtained from the human subject;
> >
> > sequencing, by next generation sequencing, the nucleic acid to generate the sequence reads; and
> >
> > genotyping at least some of the sequence reads using a multi-stage alignment, the genotyping performed by one or more computer software programs executing on at least one computer processor coupled to a computer-readable memory, the genotyping comprising:
> >
> > > assembling a contig using the at least some of the sequence reads, the contig including information about positions of the at least some of the sequence reads relative to each other or to a reference;
> > >
> > > aligning, using a first substitution probability and a first gap penalty, the contig to the reference human genome to obtain a reference alignment and storing the reference alignment in the computer-readable memory, the reference alignment indicative of first differences between the contig and the reference human genome;
> > >
> > > aligning, using a second substitution probability and a second gap penalty, the at least some of the sequence reads to the contig to obtain sequence read alignments and storing the sequence read alignments in the computer-readable memory, the sequence read alignments indicative of second differences between the at least some of the sequence reads and the contig; and
> > >
> > > genotyping the at least some of the sequence reads by identifying multiple mutations in the at least some of the sequence reads based on the first differences and the second differences, the genotyping comprising mapping the at least some of the sequence reads to the reference genome by combining the reference alignment and the sequence read alignments to determine an identity of each of the multiple mutations and its location in the human reference genome, the multiple mutations including mutations of different types including a first substitution and a first indel.

Briefly, the claimed techniques of the ’308 Patent utilize a multi-step assembly approach in which DNA sequencing reads are grouped into “contigs” and aligned to a reference human genome, using a first substitution probability and a first gap penalty, and then the original individual reads are re-aligned to the “contigs,” using a second substitution probability and a second gap penalty. The resulting alignments are then utilized to generate precise positional information regarding the locations of mutations in the sample DNA. Far from being routine or conventional, this approach

reflected a novel advance that has become widely adopted in the industry to improve the performance of DNA sequencing technology.

17. Likewise, the ’863 Patent teaches and claims a new technique for improving DNA sequencing technology by enhancing sequence read assembly. Representative claim 1 of the ’863 Patent is listed below:

> 1. A method for assembling and aligning a plurality of sequence reads having mutations of different types, the method comprising:
>
> obtaining a sample comprising a template nucleic acid;
>
> sequencing the sample to generate the plurality of sequence reads, the sequencing comprising;
>
> fragmenting the template nucleic acid,
>
> attaching the fragments to a surface of channels in a flow cell, and
>
> amplifying the attached fragments to create clusters, each cluster comprising a plurality of copies of the template nucleic acid in one of the channels in the flow cell;
>
> inputting a reference genome and the plurality of sequence reads into a computer system comprising a non-transitory memory and a processor coupled to the non-transitory memory, wherein the non-transitory memory has instructions stored thereon that, when executed by the processor, cause the processor to perform the steps of:
>
> assembling a contig from at least some of the plurality of sequence reads;
>
> identifying a plurality of contig-to-reference descriptions of the mutations by aligning the contig to a sequence of the reference genome, the mutations including a substitution and an indel;
>
> identifying a plurality of read-to-contig descriptions by aligning each of the at least some of the plurality of sequence reads to the contig; and
>
> generating a read-to-reference description by aligning at least one of the plurality of contig-to-reference descriptions with a corresponding at least one of the plurality of read-to-contig descriptions, wherein the read-to-reference description maps positional information of the mutations found in at least one of the at least some of the plurality of sequence reads relative to the sequence of the reference genome.

Briefly, the claimed techniques of the ’863 Patent utilize a multi-step assembly approach in which DNA sequencing reads are first generated from a sequencing process including fragmentation, attachment to a flow cell, and cluster amplification. The sequencing reads are grouped into “contigs” and aligned to a reference genome, and then the original individual reads are re-aligned

to the "contigs." The resulting alignments are then utilized to generate precise positional information regarding the locations of mutations in the sample DNA. Far from being routine or conventional, this approach reflected a novel advance that has become widely adopted in the industry to improve the performance of DNA sequencing technology.

18. The claimed techniques of the '308 Patent are not directed to an abstract idea or natural law, but are rather directed to a concrete technique that is used solely in conjunction with DNA sequencing technology of the kind that generates multiple independent reads. As the examiner explained in the Notice of Allowance, the claim element in the '308 Patent "of aligning contigs to a reference genome is too complex to be practical to be performed in the human mind and that limitation consequently does not recite a mental process grouping of an abstract idea." Ex. 9 at 8. Instead, the claimed invention improves upon and realizes the full potential of such DNA sequencing technology. In this regard, the claimed techniques of the '308 Patent expressly require "obtaining nucleic acid from the biological sample obtained from the human subject," and then "sequencing" "the nucleic acid to generate the sequence reads." In particular, the claimed inventions improve upon the predominant technology platform (Illumina) that was in use at the time of filing and even today, which generates DNA sequencing reads that are short and hence present particular challenges with respect to detection of certain kinds of mutations. While offering a specific improvement to DNA sequencing technology, the claimed inventions of the '308 Patent are not pertinent to other techniques for genomic analysis that produces different types of data, such as the use of microarrays.

19. The claimed combination of steps in the '308 Patent is not routine and conventional, and neither are the individual steps claimed in the '308 Patent. By way of example only, the claims of the '308 Patent recite the following steps:

aligning, using a first substitution probability and a first gap penalty, the contig to the

> reference human genome to obtain a reference alignment and storing the reference alignment in the computer-readable memory, the reference alignment indicative of first differences between the contig and the reference human genome;
>
> aligning, using a second substitution probability and a second gap penalty, the at least some of the sequence reads to the contig to obtain sequence read alignments and storing the sequence read alignments in the computer-readable memory, the sequence read alignments indicative of second differences between the at least some of the sequence reads and the contig; and
>
> genotyping the at least some of the sequence reads by identifying multiple mutations in the at least some of the sequence reads based on the first differences and the second differences, the genotyping comprising mapping the at least some of the sequence reads to the reference genome by combining the reference alignment and the sequence read alignments to determine an identity of each of the multiple mutations and its location in the human reference genome, the multiple mutations including mutations of different types including a first substitution and a first indel.

The individual step of generating "reference alignment indicative of first differences between the contig and the reference human genome," was not routine and conventional at the time, but rather represented a new approach to the assembly of DNA sequencing data. As the examiner explained in the Notice of Allowance, the claim element in the '308 Patent "of aligning contigs to a reference genome is considered to be an additional element that is not routine and conventional." Ex. 9 at 4. The same is true for the step of generating "sequence read alignments indicative of second differences between the at least some of the sequence reads and the contig," and the subsequent combination of the "reference alignment" and "sequence read alignments" to identify mutations. Specifically, "using a first substitution probability and a first gap penalty" to perform the contig-to-reference alignment and "using a second substitution probability and a second gap penalty" to perform the sequence read-to-contig alignment represent approaches that were not routine and conventional at the time. Thus, the identification of multiple mutations "of different types including a first substitution and a first indel" from a combination process that considers "the first differences and the second differences" from the contig-to-reference and read-to-contig alignments was not a routine and conventional method for identifying mutations from sequence reads. None of these steps were in use prior to the claimed invention, and hence could not have been routine and conventional.

20. The claims of the '308 Patent encompass an inventive concept that improved upon the prior art. Specifically, by using the claimed technique, researchers can overcome the tradeoff in mutation detection capability that was inherent in the prior art and perform analyses that were previously thought intractable. This inventive concept is repeatedly detailed in the specification:

> By these methods, positional accuracy of reads is obtained and the limitations of a tradeoff between substitution sensitivity and deletion sensitivity are overcome. By combining data in this way, an accurate and sensitive interpretation of the nucleic acid is obtained and an accurate description of a genotype including an identity and a location of a mutation on an organism's genome is reported.

Ex. 1 at 2:55-61.

> The output of the local alignment, describing the read compared to the contig, can be combined with the output of the reference alignment, describing the contig compared to the reference. This combination gives, for any mutation detected in the nucleic acid, a description of that mutation relative to the reference genome. Wild type and mutant alleles including specific mutations can be identified. Mutation patterns previously thought to pose particular difficulty (e.g., long indels, indel-proximal substitutions, and indels near the ends of reads) are identified with fidelity. Methods of the invention can perform, with high-throughput data using existing computer power, sequencing and genotyping analyses that were previously computationally intractable.
>
> By combining information in this way, the limitations of a tradeoff between substitution sensitivity and deletion sensitivity is overcome. The output includes an accurate and sensitive interpretation of the subject nucleic. This provides an accurate description of a genotype including an identity and a location of a mutation on an organism's genome.

Id. at 4:41-60.

21. The claimed techniques of the '863 Patent are not directed to an abstract idea or natural law, but are rather directed to a concrete technique that is used solely in conjunction with DNA sequencing technology of the kind that generates multiple independent reads. As the examiner explained in the Notice of Allowance, the claim element in the '863 Patent "of aligning contigs to a reference genome is too complex to be practical to be performed in the human mind and that limitation consequently does not recite a mental process grouping of an abstract idea." Ex. 10 at 6. Instead, the claimed invention improves upon and realizes the full potential of such DNA sequencing technology. In this regard, the claimed techniques of the '863 Patent expressly require "obtaining a sample comprising a template nucleic acid," and then "sequencing the sample

to generate the plurality of sequence reads." In particular, the claimed inventions improve upon the predominant technology platform (Illumina) that was in use at the time of filing and even today and require "fragmenting" the sample, "attaching" fragments to a flow cell, and "amplifying" the attached fragments via cluster amplification. This form of amplification generates DNA sequencing reads that are short and hence present particular challenges with respect to detection of certain kinds of mutations. While offering a specific improvement to a specific DNA sequencing technology, the claimed inventions of the '863 Patent are not pertinent to other techniques for genomic analysis that produces different types of data, such as the use of microarrays.

22. The claimed combination of steps in the '863 Patent is not routine and conventional, and neither are the individual steps claimed in the '863 Patent. By way of example only, the claims of the '863 Patent recite the following steps:

> identifying a plurality of contig-to-reference descriptions of the mutations by aligning the contig to a sequence of the reference genome, the mutations including a substitution and an indel;
>
> identifying a plurality of read-to-contig descriptions by aligning each of the at least some of the plurality of sequence reads to the contig; and
>
> generating a read-to-reference description by aligning at least one of the plurality of contig-to-reference descriptions with a corresponding at least one of the plurality of read-to-contig descriptions, wherein the read-to-reference description maps positional information of the mutations found in at least one of the at least some of the plurality of sequence reads relative to the sequence of the reference genome.

The individual step of generating "contig-to-reference descriptions" that specifically includes "a substitution and an indel" was not routine and conventional at the time, but rather represented a new approach to the assembly of DNA sequencing data. As the examiner explained in the Notice of Allowance, the claim element in the '863 Patent "of aligning contigs to a reference genome is considered to be an additional element that is not routine and conventional." Ex. 10 at 6-7. The same is true for the step of generating "read-to-contig descriptions," and the subsequent combination of the "contig-to-reference descriptions" and "contig-to-reference descriptions" to

identify mutations. None of these steps were in use prior to the claimed invention, and hence could not have been routine and conventional.

23. The claims of the '863 Patent encompass an inventive concept that improved upon the prior art. Specifically, by using the claimed technique, researchers can overcome the tradeoff in mutation detection capability that was inherent in the prior art and perform analyses that were previously thought intractable. This inventive concept is repeatedly detailed in the specification:

> By these methods, positional accuracy of reads is obtained and the limitations of a tradeoff between substitution sensitivity and deletion sensitivity are overcome. By combining data in this way, an accurate and sensitive interpretation of the nucleic acid is obtained and an accurate description of a genotype including an identity and a location of a mutation on an organism's genome is reported.

Ex. 2 at 2:55-61.

> The output of the local alignment, describing the read compared to the contig, can be combined with the output of the reference alignment, describing the contig compared to the reference. This combination gives, for any mutation detected in the nucleic acid, a description of that mutation relative to the reference genome. Wild type and mutant alleles including specific mutations can be identified. Mutation patterns previously thought to pose particular difficulty (e.g., long indels, indel-proximal substitutions, and indels near the ends of reads) are identified with fidelity. Methods of the invention can perform, with high-throughput data using existing computer power, sequencing and genotyping analyses that were previously computationally intractable.
>
> By combining information in this way, the limitations of a tradeoff between substitution sensitivity and deletion sensitivity is overcome. The output includes an accurate and sensitive interpretation of the subject nucleic. This provides an accurate description of a genotype including an identity and a location of a mutation on an organism's genome.

Id. at 4:41-60.

24. In or around August 2017, Natera began selling and offering to sell its commercial liquid biopsy test for cancer diagnostic, which it refers to by the trade name Signatera™. Ex. 3 at 17 [NTRA's 2017 10-K]. On information and belief, in or around May 2019, Natera began selling or offering to sell the test for clinical use as a laboratory developed test at its CLIA laboratory operating in San Carlos, California ("CLIA laboratory"). Ex. 4 at 15 [NTRA's 2019 10-K].

25. Technical literature describing the technology underlying the Signatera™ test explains that it involves collecting tissue and whole blood samples from patients, performing analysis on them to determine somatic mutations, and generating a custom PCR panel for monitoring. *See* Ex. 5 [Signatera: A personalized, tumor-informed approach to detect molecular residual disease with high sensitivity and specificity].

26. When Natera performs the Signatera™ test, Natera infringes literally or under the doctrine of equivalents at least claim 1 of the '308 Patent. As set forth in the scientific literature, the Signatera™ test includes performing whole exome sequencing to compare the sequence from tumor tissue with that from matched whole blood to determine a set of 16 somatic single-nucleotide variants. *See* Ex. 5 [Signatera: A personalized, tumor-informed approach to detect molecular residual disease with high sensitivity and specificity]. On information and belief, Natera carries out identification of somatic mutations using the tool Genome Analysis Toolkit ("GATK") HaplotypeCaller or a method that implements a similar analysis, such as Mutect2. *See, e.g.*, Ex. 6 [https://gatk.broadinstitute.org/hc/en-us/articles/360037593851-Mutect2]. Upon information and belief, Natera carries out this process when it performs the Signatera™ test.

27. As an example, a preliminary and exemplary claim chart detailing Natera's infringement of at least claims 1 of the '308 Patent is attached hereto as Exhibit 7. This chart is not intended to limit Plaintiff's right to modify it, to provide other claim charts, or to allege that other activities of Natera infringe the identified claims, or any other claims of the '308 Patent or any other patents. Exhibit 7 is hereby incorporated by reference in its entirety. Each claim element in Exhibit 7 that is mapped to the Signatera™ test shall be considered an allegation within the meaning of the Federal Rules of Civil Procedure and therefore a response to each claim element is required.

28. When Natera performs the Signatera™ test, Natera infringes literally or under the doctrine of equivalents at least claim 1 of the '863 Patent. As set forth in the scientific literature, the Signatera™ test includes performing whole exome sequencing to compare the sequence from tumor tissue with that from matched whole blood to determine a set of 16 somatic single-nucleotide variants. *See* Ex. 5 [Signatera: A personalized, tumor-informed approach to detect molecular residual disease with high sensitivity and specificity]. On information and belief, Natera carries out identification of somatic mutations using the tool Genome Analysis Toolkit ("GATK") HaplotypeCaller or a method that implements a similar analysis, such as Mutect2. *See, e.g.*, Ex. 6 [https://gatk.broadinstitute.org/hc/en-us/articles/360037593851-Mutect2]. Upon information and belief, Natera carries out this process when it performs the Signatera™ test.

29. As an example, a preliminary and exemplary claim chart detailing Natera's infringement of at least claims 1 of the '863 Patent is attached hereto as Exhibit 8. This chart is not intended to limit Plaintiff's right to modify it, to provide other claim charts, or to allege that other activities of Natera infringe the identified claims, or any other claims of the '863 Patent or any other patents. Exhibit 8 is hereby incorporated by reference in its entirety. Each claim element in Exhibit 8 that is mapped to the Signatera™ test shall be considered an allegation within the meaning of the Federal Rules of Civil Procedure and therefore a response to each claim element is required.

COUNT I

30. Plaintiff repeats and re-alleges the foregoing paragraphs as if set forth specifically herein.

31. On October 19, 2021, the United States Patent and Trademark Office duly and legally issued U.S. Patent No. 11,149,308 B2, entitled "Sequence Assembly." A copy of the '308 Patent is attached as Exhibit 1.

32. Gregory Porreca and Caleb Kennedy are the sole and true inventors of the '308 Patent. By operation of law and as a result of written assignment agreements, Invitae obtained the entire right, title, and interest to and in the '308 Patent.

33. Natera has infringed and continues to infringe one or more claims of the '308 Patent pursuant to 35 U.S.C. § 271(a), literally or under the doctrine of equivalents, by performing within the United States without authority the Signatera™ test. As an example, attached as Exhibit 7 is a preliminary and exemplary claim chart detailing Natera's infringement of these claims of the '308 Patent. This chart is not intended to limit Plaintiff's right to modify the chart or to allege that other activities of Natera infringe the identified claims or any other claims of the '308 Patent or any other patents.

34. Exhibit 7 is hereby incorporated by reference in its entirety. Each claim element in Exhibit 7 that is mapped to Natera's Signatera™ test shall be considered an allegation within the meaning of the Federal Rules of Civil Procedure and therefore a response to each claim element is required.

COUNT II

35. Plaintiff repeats and re-alleges the foregoing paragraphs as if set forth specifically herein.

36. On October 26, 2021, the United States Patent and Trademark Office duly and legally issued U.S. Patent No. 11,155,863 B2, entitled "Sequence Assembly." A copy of the '863 Patent is attached as Exhibit 2.

37. Gregory Porreca and Caleb Kennedy are the sole and true inventors of the '863 Patent. By operation of law and as a result of written assignment agreements, Invitae obtained the entire right, title, and interest to and in the '863 Patent.

38. Natera has infringed and continues to infringe one or more claims of the '863 Patent pursuant to 35 U.S.C. § 271(a), literally or under the doctrine of equivalents, by performing within the United States without authority the Signatera™ test. As an example, attached as Exhibit 8 is a preliminary and exemplary claim chart detailing Natera's infringement of these claims of the '863 Patent. This chart is not intended to limit Plaintiff's right to modify the chart or to allege that other activities of Natera infringe the identified claims or any other claims of the '863 Patent or any other patents.

39. Exhibit 8 is hereby incorporated by reference in its entirety. Each claim element in Exhibit 8 that is mapped to Natera's Signatera™ test shall be considered an allegation within the meaning of the Federal Rules of Civil Procedure and therefore a response to each claim element is required.

DEMAND FOR JURY TRIAL

40. Pursuant to Federal Rule of Civil Procedure 38(b), Plaintiff demands a jury trial on all issues so triable.

PRAYER FOR RELIEF

WHEREFORE, Invitae prays for relief with respect to the '308 and '863 Patents as follows:

A. A judgement that Natera has infringed the '308 Patent and that the '308 Patent is valid;

B. A judgement that Natera has infringed the '863 Patent and that the '863 Patent is valid;

C. Damages or other monetary relief, including, but not limited to, costs and pre- and post-judgement interest, to Plaintiff;

D. An order enjoining Natera and its officers, directors, agents, servants, affiliates, employees, divisions, branches, subsidiaries, parents, and all others acting in active concert therewith from further infringement of the '308 and '863 Patents; and

E. Such further and other relief as this Court deems proper and just, including, but not limited to, a determination that this is an exceptional case under 35 U.S.C. § 285 and an award of attorneys' fees and costs to Plaintiff in this action.

Dated: November 21, 2021

Respectfully submitted,

FARNAN LLP

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